; Sequence 24, Application US/08879338A
; Patent No. 6063906
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha
; TITLE OF INVENTION: Subunit
; FILE REFERENCE: B0801/7080/ERP
; CURRENT APPLICATION NUMBER: US/08/879,338A
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: US 08/663,731
; EARLIER FILING DATE: 1996-06-14
; EARLIER APPLICATION NUMBER: US 08/199,776
; EARLIER FILING DATE: 1994-02-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-08-879-338-24

Query Match 2.0%; Score 8; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        385 EDEEEEEE 392
              ||||||||
Db          1 EDEEEEEE 8
```

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; Sequence 24, Application US/08199776
; Patent No. 5594120
;  GENERAL INFORMATION:
;    APPLICANT:  Brenner, Michael B.
;    APPLICANT:  Parker, Christina M.
;    TITLE OF INVENTION:  No. 5594120el integrin alpha subunit
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield and Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/199,776
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7020
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  synthetic peptide
US-08-199-776-24

  Query Match              2.0%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        385 EDEEEEEE 392
              ||||||||
Db          1 EDEEEEEE 8
```

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ID   Q8TAD8      PRELIMINARY;      PRT;   396 AA.
AC   Q8TAD8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Smad nuclear interacting protein (Smad nuclear-interacting protein
DE   1).
GN   SNIP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20347038; PubMed=10887155;
RA   Kim R.H., Wang D., Tsang M., Martin J., Huff C., Caestecker M.P.,
RA   Parks T.W., Meng X., Lechleider R.J., Wang T., Roberts A.B.;
RT   "A novel smad nuclear interacting protein, SNIP1, suppresses p300-
RT   dependent TGF-beta signal transduction.";
RL   Genes Dev. 14:1605-1616(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Lin Y., Martin J., Gruendler C., Mach M., Meng X., Li B.-Y.,
RA   Lechleider R.J., Huff C., Kim R.H., Grasser W., Paralkar V., Wang T.;
RT   "Smad1 interaction with antizyme and proteasome beta subunit HsN3 in
RT   signal transduction of BMPs.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027040; AAH27040.1; -.
DR   EMBL; AY081909; AAL91140.1; -.
DR   InterPro; IPR000253; FHA.
DR   Pfam; PF00498; FHA; 1.
DR   SMART; SM00240; FHA; 1.
DR   PROSITE; PS50006; FHA_DOMAIN; 1.
SQ   SEQUENCE   396 AA;  45777 MW;  B183F83EC3184676 CRC64;

  Query Match             100.0%;  Score 396;  DB 4;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  396;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKAVKSERERGSRRRHRDGDVVLPAGVVVKQERLSPEVAPPAHRRPDHSGGSPSPPTSEP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKAVKSERERGSRRRHRDGDVVLPAGVVVKQERLSPEVAPPAHRRPDHSGGSPSPPTSEP 60

Qy         61 ARSGHRGNRARGVSRSPPKKKNKASGRRSKSPRSKRNRSPHHSTVKVKQEREDHPRRGRE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARSGHRGNRARGVSRSPPKKKNKASGRRSKSPRSKRNRSPHHSTVKVKQEREDHPRRGRE 120

Qy        121 DRQHREPSEQEHRRARNSDRDRHRGHSHQRRTSNERPGSGQGQGRDRDTQNLQAQEEERE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRQHREPSEQEHRRARNSDRDRHRGHSHQRRTSNERPGSGQGQGRDRDTQNLQAQEEERE 180

Qy        181 FYNARRREHRQRNDVGGGGSESQELVPRPGGNNKEKEVPAKEKPSFELSGALLEDTNTFR 240
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AC AAG93323;
XX
DT 13-SEP-2001 (first entry)
XX
DE Human protein HP10101.
XX
KW Human; gene therapy; tumour.
XX
OS Homo sapiens.
XX
PN WO200142302-A1.
XX
PD 14-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-JP08631.
XX
PR 06-DEC-1999; 99JP-0346863.
PR 06-DEC-1999; 99JP-0346864.
PR 08-FEB-2000; 2000JP-0031062.
PR 10-FEB-2000; 2000JP-0034090.
PR 10-FEB-2000; 2000JP-0034091.
PR 14-FEB-2000; 2000JP-0035829.
PR 14-FEB-2000; 2000JP-0035899.
PR 14-MAR-2000; 2000JP-0071161.
PR 30-MAY-2000; 2000JP-0160851.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kato S, Eguchi C, Saeki M;
XX
DR WPI; 2001-381646/40.
DR N-PSDB; AAH68608.
XX
PT Human protein originated from tumor cell line, applicable as drug,
PT reagent for studying intracellular protein networks and protein source
PT for drug screening, also encoded cDNA for gene diagnosis and gene
PT therapy -
XX
XX
CC The present sequence is a human protein. The human protein, preferably
CC originated from tumour cell line, is applicable as a drug, a reagent for
CC studying intracellular protein networks and a protein source for
CC screening proteins for binding low molecular weight drugs. The human
CC protein coding sequence is useful for gene diagnosis and gene therapy,
CC expression vectors and transformant cells for detection of ligands and
CC receptors.
XX
SQ Sequence 396 AA;

Query Match 100.0%; Score 396; DB 22; Length 396;
Best Local Similarity 100.0%; Pred. No. 0;

Late 09/890,688
20030144758A1

AC AAB61328;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human transcriptional regulator protein #28.
XX
KW Human; transcriptional regulator protein; TXREG.
XX
OS Homo sapiens.
XX
PN WO200078954-A2.
XX
PD 28-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-US16766.
XX
PR 18-JUN-1999; 99US-0140109.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Baughn MR, Azimzai Y, Tran B;
XX
DR WPI; 2001-041425/05.
XX
PT Isolated polypeptide with a human transcriptional regulator protein
PT sequence is useful for the diagnosis, prevention and treatment of
PT disorders associated with the immune, reproductive and cardiovascular
PT systems -
XX
PS Claim 1; Page 117-118; 142pp; English.
XX
CC The present invention relates to human transcriptional regulator
CC protein (TXREG) sequences. The antagonist and an agonist of the proteins
CC of the invention are used to treat disorders associated with decreased
CC or increased expression or activity of TXREG.
XX
SQ Sequence 396 AA;

Query Match 100.0%; Score 396; DB 22; Length 396;